SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: ZENECA LIMITED
        (B) STREET: 15 STANHOPE GATE
        (C) CITY: LONDON
        (D) STATE: LONDON
        (E) COUNTRY: UNITED KINGDOM
        (F) POSTAL CODE (ZIP): W1Y 6LN

    (ii) TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING

    (iii) NUMBER OF SEQUENCES: 57

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

    (v) CURRENT APPLICATION DATA:
        APPLICATION NUMBER: GB PPD

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 785 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: U-U9

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CGGCACGAGG AAAAACTANG TGAGAANGAG ATAATCGTTG ACCGAGGNAG AGAATGGCGA        60

GCGAGAAGAG CAAAATCCTG ATCATCGGGG GCACCGGGTA CATCGGCAAG TTCATCGTGT       120

TTGCGAGCGC CAGGTTAGGT AACCCTACCT TCGCTCTCGT CCGGAGCACC ACCGCCCCCG       180

CCGGCCAACC CGAGAAGGCC AAGCTCCTGA GCGACTTCCA GGCCGCCGGC GTCACCCTCG       240

TCCAGGGGGA TATNTATAAC CACGAGAGTC TGGTTAAGGC GATCAAGCTG GTGGATGTGG       300

TCATCTCCCC CGTCGGCTTC GGGCANCTGA NTGATCAGAC CAAGATCATC GACGCCATCN       360

AANAAGCCGG AGGACACATC AAGAGGTACC TTCCATCGGA GTTTGGCAAC GACGTANACC       420

GAAGCCATGC TGTGGAGCCA GCAAAGTCTA CCTTTGTCGT CAAGCAACAA ATCANAAGGG       480

CTGTTGAGGC ATCGGGTNTC CCTTACACCT TTGTATCTTC CAACTTTCTT CGGTGGGTNT       540

TTCCTCCCGG TATTATGACA GGCAGGAGCC ACTGGTCCTC CCACGGACAA GGTTGTCATC       600

TTAGGTNACG GGAACNCAAA ACGATCTTCT CNATGAANAC GACTTCCGGA CATCCCATTT       660

ANTCTTGGAT GATCCATAAC CTGAACCAGG TTCTATTTCT TAAAACTTCC NCCACTTCTT       720

NTCTCTTANC ANCTCNTTTC CCTCTTGGGA AAAAAATGTC NNCTANACTT CNAAAAGGGT       780

TTANT                                                                  785
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(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 813 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: U-U17

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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CGCGCACGAG GAAGAAAACT AGGTGAGAAN GAGATAATCG TTGACCGAGG NAGAGAATGG    60

CGAGCGAGAA GAGCAAAATC CTGATCATCG GGGGCACCGG GTACATCGGC AAGTTCATCG   120

TGTTTGCGAG CGCCAGGTTA GGTAACCCTA CCTTCGCTCT CGTCCGGAGC ACCACCGCCC   180

CCGCCGGCCA ACCCGAGAAG GCCAAGCTCC TGAGCGACTT CCAGGCCGCC GGCGTCACCC   240

TCGTCCAGGG GGATATATAT AACCACGAGA GTCTGGTTAA GGCGATCAAG CTGGTGGATG   300

TGGTCATCTC CCCCGTCGGC TTCGGGCANC TGANTGATCA GACCAAGATC ATCGACGCCA   360

TCAAAGAAGC CGGAGGACAC ATCAAGAGGT ACCTTCCATC GGAGTTTGGC AACGACGTAN   420

ACCGAAGCCA TGCTGTGGAG CCAGCAAAGT CGACCTTTGT CGTCAAGCAA CAAATCANAA   480

GGGCTGTTGA GGCATCGGGT ATCCCTTACA CCTTTGTATC TTCCAACTTC TTCGGTGGGT   540

NTTTCCTCCC GGTATTANGA CAGGCAGGAG CCACTGGTCC TCCCACGGAC AAGGTTGTCA   600

TCTTANGTGA CGGGAACACA AAAGCGATCT TTCTCAATGA ANACACATCC GGACNTNCAC   660

NATTAAAGCA GTGGATGATC CGAAAACCTG AACANGTTCT ATATCTGAAA CCTTCCGCCA   720

CTCTTGTCTC ATNACAACTC ATTTCCCTCT GGGAAAAAAA NGTCNGCAAA ACTCCNAAAA   780

GGTCTACTTC CCGGAAGAAA AATCTGAANC ANA                                813
```

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 746 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: U-U66

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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GGCACGAGGG GAAAAGGAGA TNATCGTTGA CCGAGGAGAG AATGGCGAGC GAGAAGAGCA    60

AGATCCTGAT CATCGGGGGC ACGGGGTACA TCGGCAAGTT CATCGTGTTT GCGAGCGCCA   120

GGTTAGGTAA CCCTACCTTC GCTCTCGTCC GGAGCACCAC CGCCCCCGCC GGCCAACCCG   180
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AGAAGGGCAA GCTCCTGAGC GACTTCCAGG CCGCCGGCGT CACCCTGGTC CAGGGGGATA    240

TATATAACCA CNAGAGTCTG GTTAAGGCGA TCAAGCTGGT GGATGTGGTC ATCTCCCCCG    300

TCGGCTTCGG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA    360

GGACACATCA AGAGGTACCT TCCATCGGGA GTTTGGCAAC GACGTANACC GAAGCCATGC    420

TGTGGAAGCC ANCAAAGTCG ACCTTTGTCG TCAAGCAACA AATTANAAGG GCTGTTGAGG    480

CATCGGGGAT CCCTTACACC TTTGTTATCT TCCAACTTCT TCGGTGGGTA TNTCCTCCCC    540

GTATTGGGAC AGGCANGAAC CACTGGTCCT CCCCACGGAC AAGGTTGTCN TCTTAGGTGA    600

ACGGGAACAC CAANGCGATC TTTCTCAATG AAAGACAACT CGGGACATNC CCNATTTAAC    660

CANTGGATGA TCCNANAACC TGAACAAGGT CTATTTCTGA AAACTTCNCC ATCTTCTTTT    720

TCTCATAACG AACCCNTTTN CCTCTT                                         746
```

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 795 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: U-U104

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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GGCACGAGGA AANGAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA     60

ATCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTTGC GAGCGCCAGG    120

TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG CCAACCCGAG    180

AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGGCGTCA CCCTCGTCCA GGGGGATATA    240

TATAACCACG AGAGTCTGGT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT CTCCCCCGTC    300

GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA AGCCGGAGGA    360

CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG    420

TGGAGCCAGC AAAGTCNACC TTTGTCGTCA AGCAACAAAT CANAAGGGCT GTTGANGCAT    480

CGGGTNTCCC TTACACCTTT GTATCTTCCA ACTTCTTCGG TGGGTATTTC CTCCCGGTAT    540

TANGACAGGC AGGACCACTG GTCCTCCCCA CNGACAAGGT TGTCNTCTTA GGTGACNGGA    600

ACACAAAANC ATCTTTCTCN ATGAAGACAA CTCCGGACAT ACNCNATTAA AGCNGTGGAT    660

GATCCCAAAA CCTGAACAAG TTCCTATNTC TTGAAAACTT TCCCGCCCAA CCATCCTTTN    720

GTTCTCCCNT TAAACCNAAC CTCCATTTTC CCCTCCTTGG GGAAAAAAAA AAGGTCCGGC    780

NAANAACTTC CNAAA                                                     795
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(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS: